Application No: 10585491   Version No: 2.0

Input Set:

Output Set:

Started: 2009-11-11 13:33:15.679
Finished: 2009-11-11 13:33:18.468
Elapsed: 0 hr(s) 0 min(s) 2 sec(s) 789 ms
Total Warnings: 53
Total Errors: 0
No. of SeqIDs Defined: 61
Actual SeqID Count: 61

Error code   Error Description

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W   213   Artificial or Unknown found in <213> in SEQ ID (3)

W   213   Artificial or Unknown found in <213> in SEQ ID (4)

W   213   Artificial or Unknown found in <213> in SEQ ID (5)

W   213   Artificial or Unknown found in <213> in SEQ ID (6)

W   213   Artificial or Unknown found in <213> in SEQ ID (7)

W   213   Artificial or Unknown found in <213> in SEQ ID (8)

W   213   Artificial or Unknown found in <213> in SEQ ID (9)

W   213   Artificial or Unknown found in <213> in SEQ ID (10)

W   213   Artificial or Unknown found in <213> in SEQ ID (11)

W   213   Artificial or Unknown found in <213> in SEQ ID (12)

W   213   Artificial or Unknown found in <213> in SEQ ID (13)

W   213   Artificial or Unknown found in <213> in SEQ ID (14)

W   213   Artificial or Unknown found in <213> in SEQ ID (16)

W   213   Artificial or Unknown found in <213> in SEQ ID (23)

W   213   Artificial or Unknown found in <213> in SEQ ID (24)

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W   213   Artificial or Unknown found in <213> in SEQ ID (26)

W   213   Artificial or Unknown found in <213> in SEQ ID (27)

W   213   Artificial or Unknown found in <213> in SEQ ID (28)

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              Input Set:


             Output Set:



               Started:  2009-11-11 13:33:15.679
              Finished:  2009-11-11 13:33:18.468
               Elapsed:  0 hr(s) 0 min(s) 2 sec(s) 789 ms
       Total Warnings:   53
         Total Errors:   0
  No. of SeqIDs Defined: 61
    Actual SeqID Count:  61
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Error code   Error Description

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<110>   DAVIS, SIMON

<120>   RECEPTOR MODULATORS

<130>   ISI.103

<140>   10585491
<141>   2009-11-11

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<150>   GB 0400440.4
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<170>   PatentIn version 3.2

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Thr Gly Asn Lys Ile Leu Val Lys Gln Ser Pro Met Leu Val Ala Tyr
            20   25   30

Asp Asn Ala Val Asn Leu Ser Cys Lys Tyr Ser Tyr Asn Leu Phe Ser
        35   40   45

Arg Glu Phe Arg Ala Ser Leu His Lys Gly Leu Asp Ser Ala Val Glu
    50   55   60

Val Cys Val Val Tyr Gly Asn Tyr Ser Gln Gln Leu Gln Val Tyr Ser
65   70   75   80

Lys Thr Gly Phe Asn Cys Asp Gly Lys Leu Gly Asn Glu Ser Val Thr
                85   90   95

Phe Tyr Leu Gln Asn Leu Tyr Val Asn Gln Thr Asp Ile Tyr Phe Cys
            100   105   110

Lys Ile Glu Val Met Tyr Pro Pro Pro Tyr Leu Asp Asn Glu Lys Ser
    115   120   125

Asn Gly Thr Ile Ile His Val Lys Gly Lys His Leu Cys Pro Ser Pro
    130   135   140

Leu Phe Pro Gly Pro Ser Lys Pro Phe Trp Val Leu Val Val Val Gly
145   150   155   160

Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile
                165   170   175

Phe Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met
            180   185   190

Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro
        195   200   205

Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser
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            20   25   30

Tyr Asp Asn Ala Val Asn Leu Ser Cys Lys Tyr Ser Tyr Asn Leu Phe
        35   40   45

Ser Arg Glu Phe Arg Ala Ser Leu His Lys Gly Leu Asp Ser Ala Val
    50   55   60

Glu Val Cys Val Val Tyr Gly Asn Tyr Ser Gln Gln Leu Gln Val Tyr
65   70   75   80

Ser Lys Thr Gly Phe Asn Cys Asp Gly Lys Leu Gly Asn Glu Ser Val
                85   90   95

Thr Phe Tyr Leu Gln Asn Leu Tyr Val Asn Gln Thr Asp Ile Tyr Phe
            100   105   110

Cys Lys Ile Glu Val Met Tyr Pro Pro Pro Tyr Leu Asp Asn Glu Lys
    115   120   125

Ser Asn Gly Thr Ile Ile His Val Lys Gly Lys His Leu Cys Pro Ser

Pro Leu Phe Pro Gly Pro Ser Lys Pro Leu Val Pro Arg Gly Ser Gly
145   150   155   160

Ser Lys Pro Ser Ile Ser Thr Val Pro Glu Val Ser Ser Val Phe Ile
                        165   170   175

Phe Pro Pro Lys Pro Lys Asp Val Leu Thr Ile Thr Leu Thr Pro Lys
                        180   185   190

Val Thr Cys Val Val Val Asp Ile Ser Lys Asp Asp Pro Glu Val Gln
                        195   200   205

Phe Ser Trp Phe Val Asp Asp Val Glu Val His Thr Ala Gln Thr Gln
                        210   215   220

Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Ser Val Ser Glu Leu
225   230   235   240

Pro Ile Met His Gln Asp Trp Leu Asn Gly Lys Glu Phe Lys Cys Arg
                        245   250   255

Val Asn Ser Ala Ala Phe Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
                        260   265   270

Thr Lys Gly Arg Pro Lys Ala Pro Gln Val Tyr Thr Ile Pro Pro Pro
                        275   280   285

Lys Glu Gln Met Ala Lys Asp Lys Val Ser Leu Thr Cys Met Ile Thr
                        290   295   300

Asp Phe Phe Pro Glu Asp Ile Thr Val Glu Trp Gln Trp Asn Gly Gln
305   310   315   320

Pro Ala Glu Asn Tyr Lys Asn Thr Gln Pro Ile Met Asp Thr Asp Gly
                        325   330   335

Ser Tyr Phe Val Tyr Ser Lys Leu Asn Val Gln Lys Ser Asn Trp Glu
                        340   345   350

Ala Gly Asn Thr Phe Thr Cys Ser Val Leu His Glu Gly Leu His Asn
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1               5                   10                  15


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Tyr Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Tyr Xaa Xaa Xaa
1               5                   10                  15


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<220>
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1                   5                   10                  15


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Xaa
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<210> 11
<211> 57

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ctcaacttat tcccttcaat tcaagtaaca ggaaacaaga ttttggtgaa gcagtcgccc     180

atgcttgtag cgtacgacaa tgcggtcaac cttagctgca agtattccta caatctcttc     240

tcaagggagt tccgggcatc ccttcacaaa ggactggata gtgctgtgga agtctgtgtt     300

gtatatggga attactccca gcagcttcag gtttactcaa aaacggggtt caactgtgat     360

gggaaattgg gcaatgaatc agtgacattc tacctccaga atttgtatgt taaccaaaca     420

gatatttact tctgcaaaat tgaagttatg tatcctcctc cttacctaga caatgagaag     480

agcaatggaa ccattatcca tgtgaaaggg aaacaccttt gtccaagtcc cctatttccc     540

ggaccttcta agcccttttg ggtgctggtg gtggttggtg gagtcctggc ttgctatagc     600

ttgctagtaa cagtggcctt tattattttc tgggtgagga gtaagaggag caggctcctg     660

cacagtgact acatgaacat gactccccgc cgccccgggc ccacccgcaa gcattaccag     720

ccctatgccc caccacgcga cttcgcagcc tatcgctcct gacacggacg cctatccaga     780

agccagccgg ctggcagccc ccatctgctc aatatcactg ctctggatag gaaatgaccg     840

ccatctccag ccggccacct cagcccctgt tgggccacca atgccaattt ttctcgagtg     900

actagaccaa atatcaagat cattttgaga ctctgaaatg aagtaaaaga gatttcctgt     960

gacaggccaa gtcttacagt gccatggccc acattccaac ttaccatgta cttagtgact    1020

tgactgagaa gttagggtag aaaacaaaaa gggagtggat tctgggagcc tcttcccttt    1080

ctcactcacc tgcacatctc agtcaagcaa agtgtggtat ccacagacat tttagttgca    1140

gaagaaaggc taggaaatca ttccttttgg ttaaatgggt gtttaatctt ttggttagtg    1200

ggttaaacgg ggtaagttag agtaggggga gggataggaa gacatattta aaaaccatta    1260

aaacactgtc tcccactcat gaaatgagcc acgtagttcc tatttaatgc tgttttcctt    1320

tagtttagaa atacatagac attgtctttt atgaattctg atcatattta gtcattttga    1380

ccaaatgagg gatttggtca aatgagggat tccctcaaag caatatcagg taaaccaagt    1440

tgctttcctc actccctgtc atgagacttc agtgttaatg ttcacaatat actttcgaaa    1500

gaataaaata gttc                                                      1514


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tacgacaatg cggtcaacct tagctgcaag tattcctaca atctcttctc aagggagttc   180

cgggcatccc ttcacaaagg actggatagt gctgtggaag tctgtgttgt atatgggaat   240

tactcccagc agcttcaggt ttactcaaaa acggggttca actgtgatgg aaaattgggc   300

aatgaatcag tgacattcta cctccagaat ttgtatgtta accaaacaga tatttacttc   360

tgcaaaattg aagttatgta tcctcctcct tacctagaca atgagaagag caatggtacc   420

attatccatg tgaaagggaa acacctttgt ccaagtccgc tatttcccgg accttctaag   480

cccctggtac ccagggggtag tggtagtaag cctagcataa gtacagtccc agaagtatca   540

tctgtcttca tcttcccccc aaagcccaag gatgtgctca ccattactct gactcctaag   600

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gtagatgatg tggaggtgca cacagctcag acgcaacccc gggaggagca gttcaacagc   720

actttccgct cagtcagtga acttcccatc atgcaccagg actggctcaa tggcaaggag   780

ttcaaatgca gggtcaacag tgcagctttc cctgcccgca tcgagaaaac catctccaaa   840

accaaaggca gaccgaaggc tccacaggtg tacaccattc cacctcccaa ggagcagatg   900

gccaaggata aagtcagtct gacctgcatg ataacagact cttccctga agacattact   960

gtggagtggc agtggaatgg cagccagcg gagaactaca gaacactca gcccatcatg   1020

gacacagatg gctcttactt cgtctacagc aagctcaatg tgcagaagag caactgggag   1080

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aagagcctct cccactctcc tggtaaataa   1170

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Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly Lys Ala Thr Glu
                20   25   30

Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val
        35   40   45

Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp Asp
    50   55   60

Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr Ile
65   70   75   80

Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu
                85   90   95

Leu Met Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly Asn Gly Thr Gln
                100   105   110

Ile Tyr Val
        115

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                20   25   30

Met Gln Leu Leu Lys Gly Gly Gln Ile Leu Cys Asp Leu Thr Lys Thr
        35   40   45

Lys Gly Ser Gly Asn Thr Val Ser Ile Lys Ser Leu Lys Phe Cys His
    50   55   60

Ser Gln Leu Ser Asn Asn Ser Val Ser Phe Phe Leu Tyr Asn Leu Asp
65   70   75   80

His Ser His Ala Asn Tyr Tyr Phe Cys Asn Leu Ser Ile Phe Asp Pro
                85   90   95

Pro Pro Phe Lys Val Thr Leu Thr Gly Gly Tyr Leu His Ile
                100   105   110

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Ala Thr Phe Thr Cys Ser Phe Ser Asn Thr Ser Glu Ser Phe Val Leu
            20                  25                  30

Asn Trp Tyr Arg Met Ser Pro Ser Asn Gln Thr Asp Lys Leu Ala Ala
        35                  40                  45

Phe Pro Glu Asp Arg Ser Gln Pro Gly Gln Asp Cys Arg Phe Arg V
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